

ALLOWED CLAIMS/ TDJ

1. A method for identifying a non-human primate polynucleotide sequence encoding a polypeptide, wherein said polypeptide is or is suspected of being associated with enhanced resistance to hepatitis C virus (HCV) infection in the non-human primate, comprising the steps of:
  - a) comparing non-human primate polypeptide-coding polynucleotide sequences to polypeptide-coding polynucleotide sequences of a human, wherein said non-human has an enhanced resistance to HCV infection relative to the human; and
  - b) selecting a non-human primate polynucleotide sequence that contains a nucleotide change as compared to the corresponding sequence of the human, wherein said change is evolutionarily significant.
2. The method of claim 1 wherein the non-human primate is selected from the group consisting of chimpanzee, bonobo, gorilla and orangutan.
3. The method of claim 2 wherein the non-human primate is chimpanzee.
4. The method of claim 1, wherein the evolutionary significance of the nucleotide change is determined by the ratio of the non-synonymous substitution rate ( $K_A$ ) to the synonymous rate ( $K_S$ ) of the nucleotide sequence.
5. The method of claim 4 wherein the  $K_A/K_S$  ratio is greater than 1.0.
6. The method of claim 4 wherein the  $K_A/K_S$  ratio is about 1.5.

7. The method of claim 1 wherein the non-human polynucleotide sequence is chimpanzee p44 exon 2 or a fragment thereof of between about 18-225 nucleotides and containing at least one evolutionarily significant nucleotide change.

8. A method of identifying target sites on human p44 exon 2 polypeptide which may be suitable for therapeutic intervention, comprising identifying as target sites those amino acids in the human p44 exon 2 that correspond to chimpanzee p44 exon 2 evolutionarily significant nucleotide changes identified according to the method of claim 1.